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OM protein - nucleic search, using *frame\_plus\_p2n* model

Run on: February 26, 2003, 19:53:56 ; Search time 3193 seconds  
(without alignments)  
5897.123 Million cell updates/sec

Title: US-09-677-653A-50

Perfect score: 3374

Sequence: 1 MGDAVGASQRPHNRGTRNV.....GKIAARVARRARRAARAN 647

Scoring table: BLOSUM62

xgapop 10.0 ; xgapext 0.5  
ygapop 10.0 ; ygapext 0.5  
fgapop 6.0 ; fgapext 7.0  
delop 6.0 ; delect 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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- 2: gb\_htg:\*
- 3: gb\_in:\*
- 4: gb\_on:\*
- 5: gb\_ov:\*
- 6: gb\_pat:\*
- 7: gb\_ph:\*
- 8: gb\_dl:\*
- 9: gb\_pr:\*
- 10: gb\_ro:\*
- 11: gb\_sts:\*
- 12: gb\_sy:\*
- 13: gb\_un:\*
- 14: gb\_vl:\*
- 15: em\_ba:\*
- 16: em\_fun:\*
- 17: em\_hum:\*
- 18: em\_in:\*
- 19: em\_mu:\*
- 20: em\_cm:\*
- 21: em\_or:\*
- 22: em\_ov:\*
- 23: em\_pat:\*
- 24: em\_ph:\*
- 25: em\_pl:\*
- 26: em\_ro:\*
- 27: em\_sts:\*
- 28: em\_un:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	3374	100.0	2478 6 AR12096	AR12096 Sequence
2	3374	100.0	2478 6 AR125097	AR125097 Sequence
3	3374	100.0	2478 6 AR159968	AR159968 Sequence
4	3374	100.0	2478 6 AX028950	AX028950 Sequence
5	3374	100.0	2478 6 AX028971	AX028971 Sequence
6	3374	100.0	2478 14 HVSOAT	L3299 Helicoverpa
7	3361	99.6	2479 6 AR12098	AR12098 Sequence
8	2207	65.4	2448 14 S43937	S43937 Capsid prot
9	436	12.9	2482 14 AF02037	AF02037 Thosea as
10	407.5	12.1	5698 14 AF451742	AF451742 Euprostet
11	386.5	11.5	6625 14 AF112884	AF112884 Nudurell
12	294	8.7	6534 6 AR159953	AR159953 Sequence
13	294	8.7	6536 6 AX028972	AX028972 Sequence
14	294	8.7	6536 6 AX028972	AX028972 Sequence
15	155.5	4.6	11659 1 AE00131	AE00131 Halopacte
16	153	4.5	151826 2 AC125378	AC125378 Mus muscu
17	148.5	4.4	11000 2 LMFLCHR31_05	Continuation (6 of
18	141.5	4.2	2663 14 EBBVBLF1	X93106 Epstein-Barr
19	140.5	4.2	8516 1 AF18515	AF18515 Pseudomon
20	140.5	4.2	1124 1 AE004995	AE004995 Halobacte
21	140.5	4.2	12041 1 AB01054	AB01054 Methanosa
22	140	4.1	161563 8 AP003076	AP003076 Oryza sat
23	138.5	4.1	139517 9 AC10546	AC10546 Homo sapi
24	138	4.1	4974 3 S83394	S83394 Insulin-Lik
25	137	4.1	11482 1 AE00876	AE00876 Deinococc
26	136.5	4.0	2787 1 SCE50	AL163677 Streptomy
27	136	4.0	37620 1 SCl16	AL033496 Streptomy
28	136	4.0	310050 1 RME603642	AL03642 Rhizobium
29	135	4.0	1891 1 SBSTRRF	X78972 S bluenisi
30	134.5	4.0	2535 9 AF152475	AF152475 Homo sapi
31	134.5	4.0	5254 9 AF152306	AF152306 Homo sapi
32	134.5	4.0	15742 1 AF012116	AF013216 Myxococcus
33	134.5	4.0	157970 9 AC005609	AC005609 Homo sapi
34	134	4.0	2661 14 AF112332	AF112332 Human her
35	133.5	4.0	10793 1 AE010748	AE010748 Methanosa
36	133.5	4.0	15274 1 AE004994	AE004994 Halobacte
37	133	3.9	1849 1 SGSTR1F	X78973 S galbani DS
38	132.5	3.9	10029 1 AE011825	AE011825 Xanthomon
39	132.5	3.9	11085 1 AE00450	AE00450 Pseudomon
40	132.5	3.9	25681 1 SAE414559	AJ414559 Saccharo
41	132.5	3.9	117096 9 AC008468	AC008468 Homo sapi
42	131.5	3.9	3221 1 HALPNSD	M24544 Halobacte
43	131.5	3.9	12730 1 AE005055	AE005055 Halobacte
44	131.5	3.9	21391 1 AB070950	AB070950 Streptomy
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RESULT 1

ALIGNMENTS

AR125096 AR125096 Sequence 47 from patent 2478 bp DNA linear PAT 16-MAY-2001  
 LOCUS DEFINITION US 6177075.  
 ACCESSION AR125096  
 VERSION 1  
 KEYWORDS SOURCE Unknown.  
 ORGANISM Insect viruses and their uses in protecting plants  
 Unclassified.  
 REFERENCE 1 (bases 1 to 2478)  
 AUTHORS Christian, P. Daniel., Gordon, K. Henrich, Julius. and Hanzlik, T. Nelson.  
 TITLE Patent: US 6177075-A 47 23-JAN-2001;  
 FEATURES Location/Qualifiers 1. .2478  
 source /organism="unknown"  
 BASE COUNT 516 a 854 c 607 g 501 t  
 ORIGIN

Alignment scores:  
 Pred. No.: 3.15e-211 Length: 2478  
 Score: 3374.00 Matches: 547  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-09-677-653A-50 (1-647) x AR125096 (1-2478)

QY 1 MetGlyAlaPheGlyValAlaSerGlnArgProHisAsnArgArgGlyThrArgAspVal 20  
 366 ATGGAGATGCTGAGTGGCGTACAGGCACCTCACACCGGCGGACCGTACACGGT 425

QY 21 ArgValAlaLysThrValThrValValAsnGlyArgAspGlnArgArgGlyThrGly 40  
 426 CGGGTCAGGCACACGGTCACCGTCACTGTTAGAGAACACACGGGTGGACCGGA 485

QY 41 ArgGlnValSerProAspSerProAspSerAspSerAspSerAspSerAspSerAsp 60  
 486 AGGCAAGTGTCTCCCTGAGCAATTACCGGTGCTGCAAGACCTCGCGCAAGCCT 545

QY 61 AspAlaAsnThrIlePheAspAlaAsnIleSerSerMetProGluPheArgAsnIlePhe 80  
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QY 81 AlanGlyLysIleAspAlanAspSerAspSerAspSerAspSerAspSerAspSerAsp 100  
 606 GCCAAGGGAAATCGACCTCGCTGATCAGTCGGTGTACTAACAGAAC 665

QY 101 ProAlaGlyIleThrGluSerAlaArgAlaValGlyGluTySerIleProAspGly 120  
 666 CCAGCGGGTGCTACAGACTCTCGCGCCGCGGGAGTACTCGAAGATCCCTGACGGC 725

QY 121 LeuValIysPheSerValAspAlaGluIleAsnGluIleIysAsnGluGlyAspVal 140  
 726 CTCGTCAGTGTCTCGTGCAGCCAGATAGAGATCTAACAGGGAGTGGCCCGTC 785

QY 141 ValThrAspValSerValProLeuAspGlyArgGlnIlePheSerIlePheSerPhe 160  
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QY 161 PrometPheArgThrAlaIleArgAlaValAlaAsnValGluAsnLysGluMetSerIle 180  
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QY 181 AspValAlaLysAspIleIleGluIlePheLeuAsnAsnIleAlaAspIlePheIlePhe 200  
 906 GACGTGTCAGACGACCTCATGGCTAACAACTCGGCCACTGGCTATGRCGTT 965

QY 201 AspSerGluIleIlePheAspPheThrAspSerPheThrIleIleArgVal 220  
 966 GCTCTGAACTGGATTAACCTACCAATGACACCACTGTCGATCCGCATCCGGTT 1025

QY 221 LeuArgProThrTyrAspValProAspProAspGluGlyLeuValAlaArgThrValSerAsp 240  
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 QY 241 TyrArgLeuThrThrValValAlaIleThrProGluValAlaAsnMetProThrIleValAspIn 260  
 Db 1086 TACGGCTCTACTATAAGCGATACATGTGAACCCACATGCCAACACTCGTGACCAA 1145  
 QY 261 GlyPheThrPheGlyGlyGlnThrValAlaLeuThrProIleSerLeuProGlnTyraspVal 280  
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 QY 381 AspGluValValValThrAsnAsnProIleGlyGlyGlySerAlaProThrPheThrVal 400  
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 QY 401 ArgValProProSerAsnAlaTyroThrAsnThrValPheArgAsnThrLeuLeuGluThr 420  
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 Db 1626 CGACCCCTCTCTGTAAGCTGACTCTGCAACTGCTGACTTGGACAGAGGGTC 1685  
 QY 441 AlanAsnProIleGlyGluIleuLeuProMetProAlaAspPheGlyGlnThrVal 460  
 Db 1686 GCCACACCCGGAGATGAGTCGGTCTCTAAAGAACACTTGCTGCTATGGTC 1745  
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 Db 1866 GACTCATCTGACCCAGAACATGTCACCCGCTCAGTCACCTCCACTCC 1925  
 QY 521 CysSerIleLeuThrLysThrArgGlyArgGlyIleuLeuAsnGluGlyIleuLeuAsp 560  
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 QY 541 PheGlyGlnPheAlaHisIleGlyLeuLeuAsnGluGlyIleuLeuAsp 560  
 Db 1986 TTGGCCAAATGCGCAGCGCGCCGCTTCAGATGGAGATCTGCTCTCGCGAC 2045  
 QY 561 AspLeuAlaIleArgLeuThrGlyValIleAspProAlaIleAspAspPheAlaAlaVal 580  
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 Db 2166 ATCAGTCTGCTGGCAGACTGGCTCCGCGCTCTCGCCCTCGGAAGCTACCC 2225  
 QY 621 GlyLeuLeuMetSerValProGlyLysIleAlaAlaArgValGalaArgGalaArg 640  
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 Db 2226 GGACGCTCATGAGCTGACCGGGAGATGCCCGCGTCCCGCCGCCGAGGCC 2285  
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RESULT 3

AR15968

LOCUS AR15968

DEFINITION Sequence 1 from patent US 6251654.

ACCESSION AR15968.1

VERSION GI:16222852

KEYWORDS

SOURCE Unknown.

ORGANISM

REFERENCE

AUTHORS Gordon, R. Heinrich, and Hamzlik, T. Nelson.

TITLE Modified small RNA viruses

JOURNAL Patent: US 6251654-A 1 26-JUN-2001;

FEATURES

source 1. . 2478

BASE COUNT 516 a 854 c 607 g 501 t

ORIGIN

Alignment Scores:

Pred. No.: 3.15e-211 Length: 2478

Score: 337.00 Matches: 647

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-09-677-653A-50 (1-647) x AR15968 (1-2478)

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 QY 41 ArgGlnValSerProAspAspAsnAspAspAsnAspAspAsnAspAsnAspAsp 60  
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QY 61 AspAlaAsnThrValThrPheProAlaAsnIleSerSerMetProGluPheArgAsnTrp 80  
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 Db 1806 TCCCTCACACATCCGGTTTGGCTACGGCACACGGACCTCCGGACTACAGGGCACCGT 1865  
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 Db 1866 GACTCTATGGCAGCACAGACATGCTACCGCTGTTGGCCACACTCCGCTACTCC 1925  
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RESULT 4

AX028950 AX028950 2478 bp DNA linear PAT 16-SEP-2000  
 LOCUS Sequence 1 from Patent WO9746666.  
 DEFINITION ACCESSION AX028950  
 VERSION AX028950.1 GI:10189993  
 KEYWORDS Helicoverpa armigera stunt virus.  
 SOURCE Viruses; ssRNA positive-strand viruses, no DNA stage; Tetraviridae;  
 ORGANISM unclassified Tetrviridae.  
 REFERENCE 1 (bases 1 to 2478)  
 AUTHORS Gordon, K.H. and Hanzlik, T.N.  
 TITLE Modified small rna viruses  
 JOURNAL Patent. Wo 9746666-1 11-DEC-1997;  
 COMM SCIENT IND RES ORG (AU); GORDON KARL HEINRICH (AU); HANZLIK TERRY NILSON (AU)  
 FEATURES Location/Qualifiers  
 source 1. .2478  
 /organism="Helicoverpa armigera stunt virus"  
 BASE COUNT 516 a -854 c 607 g 501 t  
 ORIGIN

Alignment Scores:  
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 Percent Similarity: 100.00% Conservativeness: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-09-677-653A-50 (1-647) x AX028950 (1-2478)

QY 1 MetGlyAspAlaGlyValAlaSerGlnAlaGlyProHisAspArgArgGlyThrArgAsnVal 20  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 366 ATGGGAGATGCTGGAGTGGCTACAGGACCTCACAGCTGCGGGAAACCGTACGCT 425  
 QY 21 ArgValSerAlaAsnThrValThrValAsnGlyArgAsnGlnArgArgArgThrVal 40  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 426 CGGGTCAGGCCAACACCGTACAGCTGACCTGCTAATGTTAGAGAAGAACACGCGTCGGACCG 485  
 QY 41 ArgGlnValSerProProAspAspAsnProLeuAlaAlaAlaLysGlnAspLeuAlaGlnSer 60  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 486 AGGCAAGTTCCTCCCTGACAAATTACCGCTGCTGCAAGACCTCCGCAAGCCT 545  
 QY 61 AspAlaAsnThrValThrProAlaAsnMetSerSerMetProGluProIlePheAsnTrp 80  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 546 GACGCCAACACCGTACCTTCCTCTAACATCTCTAGATGCGCCGAAATCCGGATTTGG 605  
 QY 81 AlanGlyGlyLysIleAspIleAspSerAspSerIleGlyIlePheIleAsp 100  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 606 GCGAAGGAAAGATGCGACCTCGACTCGGATTCATGGCTGAGCTTCAAGG 665  
 QY 101 ProAlaGlyAlaThrGluSerAlaAlaValGlyGluThrSerLysIleProAspGly 120  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 666 CCAGGGGTCACAGAGTCGCGGCCGCGCTGCGCTGCGAGTACTGGAAGATCCCGAC 725  
 QY 121 LeuValLysPheSerValAspAlaGluIleArgGluIleTerpYasNgluGluCysProVal 140  
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 Db 726 CTCGCAAGTCCTCCGCGACGCGCACTGCTGAGCCGCTCTGCACTTCAAGTTCCGCT 785  
 QY 141 ValThrAspAlaSerValProLeuAspGlyArgGlnTrpSerIleSerIlePheSerPhe 160  
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 Db 786 GTCACTGACGCTGTCGCTCCCTCGACGGCCGAGTGGACCTCTGCACTTCAAGTTCCGCT 845  
 QY 161 ProMetPheArgThrAlaThrValAlaValAlaLysValGluAsnLysGluMetSerLeu 180  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 846 CCGAATGTCAGAACGCCCTACGTCCCGTACGGGACGCTGGAGAAGATCGC 905  
 QY 181 AspValAlaAsnAspIleIleGluTrpLeuAsnAsnLeuAlaAspTrpArgTrpVal 200  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 906 GACGTGTCACGACCTCATGAGTCGCTGACATTCCTCCGACTGTGGCTTATGTCGT 965  
 QY 201 AspSerGluGlnTrpIleAsnProThrAspThrAspThrIleGluValArgVal 220  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 966 GACTCTGACAGTGGATTAACTTCAACCATGACACCACTGACTACGTCCGCATCGCGT 1025  
 QY 221 LeuAspProThrTyrAspValProAspProThrGluGlyLeuValArgThrValSerAsp 240  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 1026 CTACGTCACACTTGACGAGCTTGACGACGCCACAGGGCCTGTCGACAGTCAGAC 1085  
 QY 241 TyrAspIleThrTyrIleAsnIleThrCysGluAlaAsnMetProThrIleValAspGln 260  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 1086 TACCGCTCTACTTAAAGGCTATCATGTAAGGCAACATGCCAACACTCGTACGCA 1145  
 QY 261 GlyPheTrpIleGlyGlyIleLeuProGlnGlyGlyIleAlaProAlaGlyThrProAlaP 280  
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 Db 1146 GGCTTGTGGATGGCGGCCAGTACGCTCTCACCCGAGTAGCCTACCGTACGAGTCAGC 1205  
 QY 281 SerGluAlaThrAlaLeuHisThrLeuAlaProSerSerAlaAlaAlaLeu 300  
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 Db 1206 AGCGAGGCCACGCCTGACACTTGACCTTCGCCAGACATCGCCGCCGCTGAC 1265  
 QY 301 AlaPheIleTrpAlaGlyIleLeuProGlnGlyGlyIleAlaProAlaGlyThrProAlaP 320  
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 Db 1266 GCGTTGTGGAGGTTGCCACAGGGGACTCGGCCCTGCCAGGACTCCAGCTGG 1325

ACCESSION	AX028971	VERSION	AX028971.1	GI	10190009
KEYWORDS					
SOURCE	Helicoverpa armigera stunt virus.				
ORGANISM	Viruses; ssRNA positive-strand viruses, no DNA stage: Tetraviridae; unclassified Tetraviridae.				
REFERENCE	1 (bases 1 to 2478)				
AUTHORS	Gordon,K.H. and Hanzlik,T.N.				
TITLE	Modified small rna viruses				
JOURNAL	Patent: WO 9746665-A 22 11-DEC-1997; COMN SCIENT IND RES ORG (AU) ; GORDON KARL HEINRICH (AU) ; HANZLIK TERRY NELSON (AU)				
BASE COUNT	501 a 607 c 854 g 516 t				
FEATURES	Location/Qualifiers				
source	1. .2478 /organism="Helicoverpa armigera stunt virus" /db_xref="taxon:37206"				
ORIGIN					
Alignment Scores:					
Pred. No.:	3.15e-211	Length:	2478		
Score:	3374.00	Matches:	647		
Percent Similarity:	100.00%	Conservative:	0		
Best Local Similarity:	100.00%	Mismatches:	0		
Query Match:	100.00%	Indels:	0		
DB:	6	Gaps:	0		
US-09-677-653A-50 (1-647) x AX028971 (1-2478)					
QY	1 MetGlyAspAlaGlyValAlaAspGlnAspProHisAsnArgArglyThrArgAsnVal 20				
Db	1746 CACTCCAAATCGGAAACCCGGTTTCAGCTCACGGCAGCCAGCTTGGGCGCTT 1805				
QY	441 AlaAsnAsnProLysIleGluGlnSerLeuLeuIysGluThrIleGlyGlyCystYrLeuVal 460				
Db	1626 CGACCCGCTCTGCTGAGCTGCAACTCCTATGCCACTCTGCTGACTTGTGACAGCGTC 1685				
QY	481 SerPheAsnAsnProGlyTYrGluArgThrArgAspIleProAspThrThrGlyIleArg 500				
Db	1806 GCCACACACCCGAGATCGGAGAGTCGCTCTCTAAAGAACACTTGCGTCATTTGGC 1745				
QY	461 HisSerLysMetArgAsnProValPheGlnIleThrProAlaSerSerPheGlyAlaVal 480				
Db	501 AspSerPheAspGlnAsnMetSerThrAlaValAlaIleAlaIlePheArgSerLeuSerHisSer 520				
QY	482 SerGlyAspSerGlyValAlaAspGlnAspProAsnGlyAsnGlyAsnGlyAsnGlyAsnVal 560				
Db	1866 GACTCAGTCGACGAGACATGPRCAACGGCTGPGCCACTTCGCTCACTCCTCCACGCC 1925				
QY	521 CysSerIleValThrLysThrYrGlyIleGlyValGluGlyValThrAsnValAsnThrPro 540				
Db	1806 TCTTCACACAAACCGGTTATGAGCGCACACCGGACCTCCGGACTACATGCGATCCGT 1865				
QY	541 PheGlyGlnPheAlaIleAsnIleLeuLeuIysAsnGluGluIleLeuIysAsnIleAsp 560				
Db	1986 TTCGGCCAAATTCGGCCACGGGGCTCTCAAGATGAGGAGATCCCTGCGCTGGCGCAC 2045				
QY	561 AspLeuIleThrArgLeuThrIleGlyValIysProAlaIleAspAsnGluGluIleLeuIysAsnIleAsp 580				
Db	2046 GACCTGGCCACCGTCACAGTGCTTACCCGGCACTGAACTTCGGCGCCGGCT 2105				
QY	581 SerAlaPheIleAlaAsnMetLeuSerSerValLeuIysSerGluAlaIleSerSerIle 600				
Db	2106 TCTGCCCTCGCCGCAACATGCTGCTCCGGCTCTGAGTCGGAGGCAACGCTCCATC 2165				
QY	601 IleLyserValGlyGluThrAlaValGlyIleAlaIleGlnSerGlyIleAlaIleAspIleLeuIysLeu 620				
Db	2166 ATCAAGTCGTTGGCGAGACATCCGGTGGGGCTCAGTCGGCCCTCGCGAGCTACCC 2225				
QY	641 ArgGalaAlaIleArgAla 647				
Db	2286 CGCCGGCCGCTCGGCCAT 2305				
RESULT	5				
DEFINITION	Sequence 22 from Patent WO9746666.	2478 bp	DNA	linear	PAT 16-SEP-2000
LOCUS	AX028971				

QY	221	LeuArgProThrTyrAspValProAspProthrlgluGlyLeuValArgThrValSerAsp	240	QY	581	SerAlaPheAlaAlaAsnMetLeuSerSerValLeuLysSerGluAlaThrSerSerIle	600
Db	1453	CTACGTCCAACCTACAGAGCTTCGAGCCCCAACAGAGGGCTTGTGCGCACAGTCAGAC	1394	Db	373	TCTGCCTCTGCCGCCAGATGCTGCCCGCTGAGTCGGGAAAGCTCTCCATC	314
QY	241	TyrArgLeuThrTyrIleAspAlaIleThrCysGluAlaAsnMetProThrIleAlaIle	260	QY	601	TleIysserValGlyGluLhrAlaIvalGlyAlaAlaGlnSerGlyLeuAlaIysLeu	620
Db	1393	TACCGCCCTCACTTATAAGGCCAACATGCCAACACTCGTGAGCAA	1334	Db	313	ATCAGTCGGTGGAGACTGCGCTCCGGCGCTCTGTCGGCCGCTCGGAGCTACCC	254
QY	261	GlyPheTerPheIleGlyGlyIleGlyIleAlaLeuThrProThrSerIleProGln	280	QY	621	GlyLeuLeuMetSerValProGlyLysIleAlaAlaArgAlaArgArgAlaArg	640
Db	1333	GCGCTTGGATGGCGGCCAGTAGCTTACCGCACTGACCTACGGCACTAGCTACGGAGTC	1274	Db	253	GGACTGCTATGAGTGTACCGAGAAGATGGCGCCGCTGCGGCCGCGCCGAGCGGC	194
QY	301	AlaPheValTrpAlaGlyIleProGlnGlyIleThrAlaProAlaGlyThrProAlaIle	320				
Db	1213	GGCTTGTGTTGGCCAGGTGGCACAGGGTGGCTCGGCCACTCGGCCCTGG	1154				
QY	321	GluGlnAlaSerSerGlyGlyIleThrLeuThrPheAlaIleGlyIleAlaIle	340				
Db	1153	GACGAGGATCCUGGGGGCTACCTCACCTGCGCCACAGGTACTCCACCT	1094				
QY	341	GlySerValSerValSerGlyIleProGluAlaIleGlyIleAspProAspAsp	360				
Db	1093	GGCTCCGGTAGCTACGTTCTCTGGAGGTTCGCCCTGAGCGCTAGACCCGAAACG	1034				
QY	361	GlySerTerPheAspPheAlaSerAlaIleAlaIleGlyIleAspThrVal	380				
Db	1033	GGCTCTGGACCACTCGCTCGAGGAGACCGTCACTTCCGGCAGRCGCGTC	974				
QY	381	AspGluValValValIleAsnAsnProAlaGlyGlyIleSerAlaProThrVal	400				
Db	973	GAGGAGGGCTTGTCGACCAACCCCCGGGGCGCAGGSCCCACCTTCACCGT	914				
QY	401	ArgValProProSerAspAlaIleThrAsnThrValIleAsnThrLeuGluThr	420				
Db	913	AGACTGCCCTCTCAAAAGCTTACACCAACACCGAGCTCTAGACCTCTAGAGCT	854				
QY	421	ArgProSerSerArgArgLeuGluLeuIleProMetProAlaAspPheGlyIle	440				
Db	853	CGAACCTCTCTCGTAGCTCGACTCCATGCCACCTCTGACTCTGACTCTGTC	794				
QY	441	AlaAsnAsnProIleGluGlnSerIleLeuIleLysGluThrIleGlyCysIle	460				
Db	793	GGCTCTGGCTTCCGACTCTGACTCTGACTCTGACTCTGACTCTGACTCTGTC	734				
QY	461	HisSerLysMetArgAspProValPheIleLeuThrProAlaSerSerPheIyAla	480				
Db	733	CACTCCAAATGGAAACCCGGAGATGAGAAGTCACGCCAGCCAGCTTGGCGCGGT	674				
QY	481	SerPheAsnAsnProGlyIleGluIleAspIleProAspPheThrGlyIleArg	500				
Db	673	TCCCTTCACAACTCGGGTTATGAGCCACACCGACCTCCGACTACGTCATCGT	614				
QY	501	AspSerPheAspGlnIleAsnMetSerThrAlaValAlaIleIlePheArgSer	520				
Db	613	GACTCATGCGACAGACATGTCACCGCTGCGCCACTCGCTACTCCACCTC	554				
QY	521	CysSerIleLeuValThrLysThrArgGlyIleGlyIleAspAsnValAsnThr	540				
Db	553	TGCGATGATCGTCACTAAGCTTACCGAGCTTACCGGTTGGAAAGGCCACGGCT	494				
QY	541	PhgIgYIleIleAlaIleAlaIleAlaIleLeuLeuAsnGluIleCysteIleAsp	560				
Db	493	TTCGGCCGATTCGCGACAGCGGGCTCCACAGATGAGGAGAACCTCTGCGCGAC	434				
QY	561	AspLeuAlaThrArgLeuThrGlyIleIlePheAlaIleAspIleLeuLeuAsp	580				
Db	433	GAACCTGGCCACCGCTCACAGCTTACCGCCACTGAACTTCGCGCCGCGGT	374				
				FEATURES			
				Source			
					Location/Qualifiers		
					1.	1..2478	
							organism="Helicoverpa armigera stunt virus"
							/isolate="black mountain"
							/clone="hasvRNA2,"
							/db_xref="txon:37206"
				5'UTR			
				stem_loop			
					1.	1..50	
							/note="stem loop which has hexamer sequence, gguaaa, in same place on a stem loop structure on RNA; putative"
							/function="unknown"
				gene			
					283.	..156	/gene="p17"
					283.	..756	/gene="p17"
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							/function="unknown"
							/note="has PEST characteristics, makes tube-like structures when expressed in bacteria, unstable when expressed in baculovirus; start codon in poor context so is poorly expressed if at all; putative"
							/codon_start=1
							/protein_id="AAC77884.1"
							/ab_xref="GI:6050504"
							/translation="MSHTAHISITLPGYTIALIPEPEAGWEMIWRHRSLDTVAE
							PTYFGSPPTPSMVEITNGPGEKGKPLPLTSPLHKTSLKALTTPSPSPSPLSIA
							PTNSIGKRSRSPSPISAGTSITLQRVLSRAPSSAISTRSLASSSSPSTQR"
				gene			
					366.	..2309	/gene="p17"
							/gene="p17"
							/standard_name="BaSV coat protein"
							/note="coat protein for BaSV, forms T=4 capsids with 240 copies of protein per capsid, upon assembly into particle is cleaved at N/P at residue positions 575-76"
				CDS			/evidence=experimental









mat_peptide	88	RTYTFLNRSQSSVINSVLPVQTYTQYRKNNGTLYANGDTLRFQTERDGGTIVRQPSA KTCVFOKEGEVYRQD1WQPVYNTPASRYAPRVEVNAITDALSANGTIRDAD SNGFALCHMISPLACRPAKIKERFEAVPGRSWPGFATSPPKDVEALTSRV MDLEPFAMPFLNGWPLFSKVLSIVRKPALRTASNYAETVAGCVDQAGVTKV ETYGRGRCAAMDITLQQ"	Db	1038 AGAGGAGTGGCCGGCTTCAACATATAGTGGAGACTGGCCGAC----- 1086
mat_peptide	88	/note="Tav-CP" /product="small capsid protein"	Db	1143 AAGGTGACAGCTTAATAGGTGTCAGGTTACAGGTGTCCTCCGTCAT 1202
mat_peptide	106	/note="Tav-CP" /product="small capsid protein"	Db	219 gValLeuArgProThrAspGlnProAspSerGluAlaAsnMetProThrLeuva 238
misc_feature	553	/note="not encapsidated in the mature virion"	Db	238 1serAspTyvArgLeuThrTylylSalieThrLysGluAlaAsnMetProThrLeuva 258
misc_feature	553	/note="alternate position for initiation methionine"	Db	1203 ARGGAGTACAGCTTCAACATATAGTGGTCAGGTTACAGGTGTCCTCCGTCAT 1262
rise_count	624	a 583 c 654 g 621 t	Db	258 IASPGInlylPheTrpIleGlyGlyInlylTyraLeuThrProThrSer----- 274
origin	1213	Gaps: 29	Db	1317 GGTATTCCTCACTCTGATCTGGGAGACCCGTTAGCTGGTGTAGTGT 1376
origin	1213	Gaps: 29	Db	293 gProSerSerAlaAlaAlaLeuAlaPheValTrpAlaGlyLeuProGlyGlyThrAla 293
origin	1213	Gaps: 29	Db	1426 -----GCACAAATCAGGAGACAGTGCACCTAAATAG 1457
origin	1213	Gaps: 29	Db	333 sasnGlyInhrhPheProAlaGlyLeuProGlyGlyThrAla 353
origin	1213	Gaps: 29	Db	1458 GTCAGGTTCTGTTGATATAAT-----AGITCAGTCCTTCCCAG-----GTGAC 1499
origin	1213	Gaps: 29	Db	353 uGluArgTyraProAsnAspGlySerTrpThrAspPheAlaSerAlaGlyAspThrVa 373
origin	1213	Gaps: 29	Db	1500 TCAAGGTTTACCGTTTATAATGG-----GACATATGCTGTAGTGTACCT 1550
origin	1213	Gaps: 29	Db	313 aProAlaGlyThrProAlaTrpGluGlnAlaSerSerGlyGlyItyLeuThrProGly 333
origin	1213	Gaps: 29	Db	373 lThrPheArgInValalaValAspGluValValThrAsnAsnProAlaGlyGlyGly 393
origin	1213	Gaps: 29	Db	1551 TCGCTTCAG-----CTGACTGAGGGATCTGCTGIGT-----1584
origin	1213	Gaps: 29	Db	393 ySerAlaProThrPheThrValArgValProProser-----AsnAlaTyrrhAs 410
origin	1213	Gaps: 29	Db	1585 -----TACACAGTCGGCTCTCAAAGTCCGCTGAGGTACCACTTTACCAA 1631
origin	1213	Gaps: 29	Db	410 n-----ThrValPheArgAsn-----415
origin	1213	Gaps: 29	Db	1632 TATAGGTTCCGCTTCGACAAACGACAGCCAGCAGCTTAAACACAGATAGCGGCT 1691
origin	1213	Gaps: 29	Db	416 ---ThrIleLeuLeuLysThrArgProSerSerGlyLeuGlu---LeuProMetProPro 433
origin	1213	Gaps: 29	Db	1692 TGGAGTCCTCTGGAAGGAGGCTGTCAGCAGTCGGCTTAATATGCCGACTCTACCTCC 1751
origin	1213	Gaps: 29	Db	433 oalaAspPheGlyGlyItyLysThrValAlaAsnAsnProLysLeuGluGlnSerLeuLeuThrGly 453
origin	1213	Gaps: 29	Db	1752 TTTTACTCAATGAGATTGATGAGCAACGCCGAAACGCTGTCCTCCAAATAAMAGA 1811
origin	1213	Gaps: 29	Db	453 uThrLeuGlyCysTyreLeuValHisSerLysMetAspAsnProValPheGlnLeuThrPr 473
origin	1213	Gaps: 29	Db	1812 a-----GGTGGTTTTATGTCAGGCCAGGATTTGCGACGCCGTTGACATATGACACC 1865
origin	1213	Gaps: 29	Db	493 -LeuProAspTyrrhCly---IleAspSerPheAspGlnAsnMetSerThrAla 511
origin	1213	Gaps: 29	Db	1920 ATTAATTCACCACTGGCTGACTGACTGACTGACTGCTTGTGCTTGTGCTTGTGCTT 1979
origin	1213	Gaps: 29	Db	511 lalaHSpheArgSerLeuSerHisSerCysSerLeuValThrLysThrTyGlnGlyTr 531



Db 4188 ATCTGGGACCCCTGGTATAATCCGCACTAATTATGGAGACTCCGTTCTGTGATGCC 4247  
 Qy 172 AsnValGluAsnLysGluMetSerIleuAspValValAsnAspLeuIleuGluTrpIleuAsn 191  
 Db 4248 GCACTGAGGAATGCTGAATAATCCGATTCATCTCTAGATGAGGTAGCTCGGCTTCAC 4307  
 Qy 192 AsnLeuAlaAspTrpArgTyValValAspSerGluInTrpIleuAsnAspLeuSerIleuAsn 211  
 Db 4308 ATTATGCTGGAGATGTAATTAGCTCTACCCGAATGGTTCAGACCTTGAGGG 4367  
 Qy 212 ThrIleuTyValArgValArgValLeuArgProThrTyValAspProAspProThr 231  
 Db 4368 GCCCTGATGG--TCCATCCAGGGTGGACGGCTTAATAGGGCTCCACCTCCAGT 4424  
 Qy 232 Glu--GlyLeuValArgThrValSerAspTyArgLeuThrTyLysAlaIleuThrCys 250  
 Db 4425 GATACGGGGTCTCCTATATCACTGATTCGGATGGGATTACTGTG 4484  
 Qy 251 GluAlaAsnMetProThrLeuValAspGluIleuPheTrpIleuGlyGluGlyInTyAlaLeu 270  
 Db 4485 TCTTCACACCCCACTCTTAAATCAGGATGGTGGTGCACAGTT 4538  
 Qy 271 ThrProThrSer-----LeuProGlnTyrsValSerGlu----- 282  
 Db 4539 AACCCCACACTGAGACAGGAGTAGTACCCATCTGAGTCGGGACTCGATG 4598  
 Qy 283 -----AlaTyAlaLeuHisThr-----LeuThrPheAlaArgPro 294  
 Db 4599 GGGTGGTCTCGGTTTATCCATCACGICACAGATAGTACGACTTATCACCA 4658  
 Qy 295 SerSerAlaAlaAla-----LeuAlaPheValTrpAlaGlyLeuPro 308  
 Db 4659 GGGGGGGAGGTGCCAGAATACCTCACGTCATGCCATAGAGGCCCTGCTGIAATT 4718  
 Qy 309 GluGlyGlyIleuAlaProAlaGlyThrProAlaTrpGluGlnAlaSerGlyGlyTyr 328  
 Db 4719 ATTAGCTCGGTTCTCCCTGCTACTCAAGTTACCGT-----TTT 4760  
 Qy 329 LeuThrTrpArgIleuAsnGlyTyThrThrPheProAlaGly--SerValSerTyValLeu 347  
 Db 4761 TTA-----AATGGAGACAGCTATGCGAGTGGGACTCCCTCCATAT----- 4802  
 Qy 348 ProGluGlyPheAlaLeuGluArgTyrAspProAsnAspGlySerTrpAspHeAla 367  
 Db 4803 -----CAGTTACGGAGCGAGAC 4820  
 Qy 368 SerAlaGlyAspThrValThrPheArgGlnValAlaValAspGluIleuValAlaAsn 387  
 Db 4821 TCAAGGGGTTACAGTC-----TATCAGCAAGGTCACTGATGGTACGACCTTACAAT 4877  
 Qy 388 AsnProAlaGlyGlyGlySerAlaProThrPheThrValArgValProProSerAla 407  
 Db 4878 -----ATGGCCGCCGCGAGACAATGCGGCCCATCTGGCACT 4919  
 Qy 408 TyrThrAsnThr-----AlpHeaGlnThrIleuLeuGluThrAspProSer 423  
 Db 4920 TCAACCGCTCTGGGGTTCTCCTAGAGGTGATTTGGCCGAGCTGTGAAT 4979  
 Qy 424 SerArgArgLeuGluIleuProMetProProAlaAspPheGlyGluThrValAlaAsn 443  
 Db 4980 ATG-----TAACTTACGCCCTTACCCAGCTGATGCAACAGACC 5027  
 Qy 444 ProLysIleGluIleuSerLeuIleuGluIleuThrLeuGlyCysTyIleuValHisSerIleu 463  
 Db 5028 CCAAAGCAGCTGTGTTCCAGATCAAAGG-----GGGGTTTATGCGGCCAGAT 5081  
 Qy 464 MetArgGlnProValPheGlnLeuThrProAlaSerSerGlyAlaValSerIleuAsn 483  
 Db 5082 GTTGGCAACCCGCTATAATGACCCGAGCCGCTATGCCCCGGTCGATGIG 5141  
 Qy 484 AsnProGlyIleuGluArgThrArgAspLeuProAspTyThrGly--IleArgAspSer 502  
 Db 5142 TCG---GGAGCAATACTTTAGATAGCCGTTAACTCTCTGTTAGGAACTATCCGGATACA 5198

Qy 503 PheAspGlnAsnMetSerThrAlaValAlaHisPheArgSerLeuSerHisSerCysSer 522  
 Db 5199 GCAGACCTCAACTATGGGTTGGCCTGGTCACATCACCTCGATACCGCTGGCGTGGCC 5258  
 Qy 523 IleValThrLysThrTyArgGlyIleuPheTrpIleuAsnAspLeuSerIleuAsn 542  
 Db 5259 CCTTTATTAAAGCTGAGATGCGCTTGAGGGTGGCCAGCTGGACTCTCCCTGGGG 5318  
 Qy 543 GlnPheAlaIleuAlaGlyLeuLeuIleuGluIleuLeuCysLeuAlaAspAspLeu 562  
 Db 5319 CTTTGGCCACCTCCACTCCCAAGGAGTGGTGGACCATATACCGACGGTC 5378  
 Qy 563 AlaThrArgLeuThrGlyValTyProAlaThrAspAsnPheAlaAlaIleuSerAla 582  
 Db 5379 ATGACTTAGACCTTGGCATGCCATAGCTGGCTGCTATAATGGTGGGCCCTGATGTC 5438  
 Qy 583 PheAlaAlaAsnMetLeuSerSerValSerValLeuIleuGluIleuAsnAlaValSerAla 602  
 Db 5439 AAATCATCAATATAGTACGCAAGGTCTCGAGGRCCTCCGACAGCAGAACCTGCT 5498  
 Qy 603 SerValGlyGluThrIleuValGlyIleuAlaAlaGlnSerGlyIleuAlaLysLeuProGlyLeu 622  
 Db 5499 GATGCTGCTAACGCGTGGAGGAGCCCAAGCTGGTGGCACC----- 5543  
 Qy 623 IleMetSerValProGlyLysIleAlaAlaArgValArgAlaArgGlyArg 642  
 Db 5544 -----CGAGTTATGAGAGTGGGGGGGGGGCTATGGGA 5585  
 RESULT 11  
 AF102884  
 LOCUS AF102884 6625 bp RNA linear VRL 30-MAY-2001  
 DEFINITION Nudaurelia capensis beta virus complete genome.  
 ACCESSION AF102884  
 VERSION AF102884.1 GI:4028586  
 KEYWORDS  
 SOURCE Nudaurelia capensis beta virus.  
 ORGANISM Nudaurelia capensis beta virus  
 Viruses; ssRNA positive-strand viruses, no DNA stage: Tetraviridae;  
 VERSION AF102884.1  
 REFERENCE 1 (bases 1 to 6625)  
 AUTHORS Gordon,K.H., Williams,M.R., Hendry,D.A. and Hanzlik,T.N.  
 TITLE Sequence of the genomic RNA of nudaurelia beta virus (Tetraviridae)  
 JOURNAL Virology 258 (1), 42-53 (1999)  
 MEDLINE 99203183  
 PUBLMED 1029566  
 REFERENCE 2 (bases 1 to 6625)  
 AUTHORS Gordon,H.J., Williams,M.R., Hendry,D.A. and Hanzlik,T.N.  
 TITLE Direct Submission  
 JOURNAL Submitted (30-OCT-1998) CSIRO Entomology, GPO Box 1700, Canberra,  
 ACT 2611, Australia  
 FEATURES  
 source 1. . 6625  
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Qy	425 ArgArgLeuGluleuProMetProAlaAspPheGlyLhrValAlaLasnAsnPro	444	Best Local Similarity:	26.74%	Mismatches:	281
Qy	445 LysIleGluGluLeuLeuIysGluGluGluLeuLeuIysGluGluGluLeuLeuIys	464	Query Match:	8.71%	Indels:	151
Qy	5257 ArgAccATTCAGTCCAACTCAGAACGAACTGACGAACTGAGCCAAACGCC	5256	DB:	6	Gaps:	35
Qy	465 ArgAsnProValPheGlnLeuThrProAlaSerSerPheGlyAlaValSerPheAsnAsn	484	US-09-677-653A-50 (1-647) x AR159969 (1-6534)			
Db	5314 TTTCAACCGTGTTCGAAATGACAATGGCGCTATGGCGGATGGCGGATGGCGGAGGACA	5373	Qy	2 GlyAspAlaGlyAlaSerGlnAsnProHisAsnArgGlyThrAsnValArg	21	
Qy	485 ProGlyTyrGluArgThrArgAspLeuProAspTyr	500	Db	4012 GGCACACGGCCGCGCCAAACACAAACAGTCGACCGAGGAGGCCGGCTAA	4071	
Db	5374 CCG-----AGGCA--ACTGTTGTTAGTTACCCACCGGCANTGGGACTCCAG	5421	Qy	22 ValSerAlaAsnThrValThrValAsnGlyArgArgAsnGlnArgArgArgThrGlyArg	41	
Qy	501 AspSerPheAspGlnAsnMetSerThrAlaValAlaLisPheArgSerLeuSerHisSer	520	Db	4072 CTTCCCCCGTAGTCGGACCCGATT-----		4095
Db	5422 GATACCATCGAGAGCAACTCCGATAGGCGTGTGCCGATGACCGTATGCTACATCA	5481	Qy	42 GluValSerProProAspAsnPheThrAlaAlaAlaGlnAspLeuAlaGlnSerLeuAsp	61	
Qy	521 CysSerIleValThrLysThrLysGlyArgGlyLysValThrAsnValAsnThrPro	540	Db	4096 --ACCACGCCGAGGGCCACCCCGAAC		CAC 4128
Db	5482 ACCGTACCCCTACTCTCAGGTTCCGAGCTCCGAGGAACTCGCCT	5541	Qy	82 LysGlyLysIleAspLeuAsp-----SerAspSerIleGlyTyrTyrPheLeuTyr	98	
Qy	541 PheGlyGlnPheAlaHisAlaGlyLeuLeuIysAsnGluGluLeuLeuCysLeuAlaAsp	560	Db	4173 ANGGCAGCGATGATGGAGAGCCCCATGCGCACGACTAACGGATCAGCGACTAT	4232	
Db	5542 TGGGCCCTCTGCCAGTGGCACCCGACCTCCGAGGACGCGGCTAACAGTGGCGCA	5601	Qy	99 LeuAspProAlaGlyAlaSerAlaArgAlaValAlaGlyLysValGlyLysIlePro	118	
Qy	561 AspLeuAlaThrArgLeuThrGlyValTyrProAlaLeuThrAspAsnPheAlaAlaAlaVal	580	Db	4129 GCGAACACCGGGCTCAA-CCGGGTCAA-----GACACGGCAGGGGCT	4172	
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Qy	641 Arg-----ArgAlaAlaArg 645		Db	4284 GACGGCGCATACCTCAGTCACATGGGGTCAATTGGGGACCGCTGGGCCAGATAC	4343	
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RESULT 12						
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LCUCS	AR159969	6534 bp	Qy	159 Ser-PheProMetPheArgThrAlaTyrValAlaValAlaAsnValGluAsnLysGlyMet	178	
DEFINITION	Sequence 4 from patent	DNA	Db	4404 CATCTCCGGTCCTCAGGCATCGCTGTCGTCATCACACCACGACACGGA-----4460		
ACCESSION	US 6251654	linear	Qy	179 SerLeuIpsValValAsn--AspLeu-----IleGluIlePheLeuAsnLeu	193	
VERSION	AR159969.1	PAT 17-OCT-2001	Db	4461 --GTCGAGTCGACGAGCCGATCAGGGATGCGTGTGGCGAACGATG--AACACAGG	4514	
SOURCE	Unknown.		Qy	194 AlaAspTyrArgTyrValValAspSerGluGlnTrieLeuAsnPhethRAsnAspThr	213	
ORGANISM	Unclassified.		Db	4515 ACGGACTCTGACCGAACGACG-----TACCCAGTTGGGGCAAGTCGGGAAC-----GTG	4565	
REFERENCE	1 (bases 1 to 6534)		Qy	214 TyrTyrValArgIleArgLeuArgValLeuArgProThr-----TyrAspValProSpPro	230	
AUTHORS	Gordon, K. Heinrich, and Hanzlik, T. Nelson.		Db	4566 TTTCACGGTC-----CGACCGAACGGCTGACGGACGTCACCCCCG	4613	
TITLE	Modified small RNA viruses		Qy	231 ThrGlu--GlyLeuValArgThrValSerAspTyrArgLeuThrTyrLysAlaIleThr	249	
JOURNAL	Patent: US 6251654 A 4 26-JUN-2001;		Db	4614 ACTCAACTGGGTTACGGGTACTCAGGAGTTCACGTCGTCAGTCGACATCGGGCAGTCACA	4673	
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SOURCES	1. .6534 /organism="unknown"		Db	4674 GCGTACCTCAAGCACCCACTCGGATAGGGTGGGGTATCGGCTCGACATCGGGCAGTCACA	4730	
BASE COUNT	1667 a	1782 c	Qy	270 LeuThrProThr-SerLeuProGlnTyrAspValSerGluAlaTyrAlaLeuHistoleu	289	
ORIGIN	1747 g	1338 t	Db	4731 --CAACCGGACAAGAACACCAAGAGAACCCGGACATAGTAGCCGGGACACCAA	4787	
Alignment Scores:	1.56e-09	Length: 6534	Qy	290 Thr-----PheAlaArgProSerSerAlaAlaAlaLeuAlaPhe	302	
Pred. No.:	294.00	Matches: 184	Db	4788 ACGGGGGAACTGTTACAGCTCGGGGCTAGGGCGAACACTACATGACGTCGATGAGC-----4844		
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Percent Similarity:			Db	4845 ATCGGGGACCCAGGTCGAGTTCGGGGCCAGCAATCCGCTACCCACGGCTCGATGGGG	4904	



Qy 194 AlaAspTrpArgGlySerValAlaAspSerGluGlnTrpIleAsnPhenThrAsnAspThrThr 213  
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 Qy 214 TyrTrpValArgIleArgValLeuArgProThr----TyrAspValProAspPro 230  
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 Db 5467 TAGTGCAGACCTCCGAGGAGGAGTGGGGCTACAGTGCTGCAACTTGAGCGATCT 5526  
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 Db 5587 CAAGACCATAGCCGAGATACCTCGC-----TATGCGCATCA----- 5623  
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 Db 5677 TGTAGCTGAATCCACCTCGAGAGAGGCCAACGAGAGCAGGAGACG 5736  
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RESULT 14  
 AX028972/c

LOCUS AX028972

DEFINITION Sequence 23 from Patent WO9746666.

ACCESSION AX028972

VERSION AX028972.1 GI:10190010

KEYWORDS

SOURCE

ORGANISM Nudaurelia capensis beta virus.

Viruses; ssRNA positive-strand viruses, no DNA stage; Tetraviridae; Betatetravirina.

REFERENCE Sequence 23 from Patent WO9746666.

AUTHORS 1 (bases 1 to 536)

JOURNAL Gordon, K.H. and Hanzlik, T.N.

TITLE Modified small rna viruses

PATENT: WO 9746666-A 23 11-DEC-1997;

COMM: SCIENT IND RES ORG (AU); GORDON KARL HEINRICH (AU); HANZLIK TERRY NELSON (AU)

FEATURES location/Qualifiers

source 1 .6536

/organism="Nudaurelia capensis beta virus"

BASE COUNT 1338 a 1747 c 1782 g 1667 t 2 others

ORIGIN

Alignment Scores:

Pred. No.: 1.56e-09

Score: 294.00

Length: 6536

Percent Similarity: 37.50%

Matches: 184

Best Local Similarity: 26.74%

Conservative: 74

Query Match: 8.71%

Mismatches: 281

Indels: 151

Gaps: 35

US-09-677-653A-50 (1-647) x AX028972 (1-6536)

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 Db 2463 CTTCCCCCGTAGTCGACCCATT----- 2440

Qy 42 GlnValSerProProAspAsnPhenThrAlaAlaAlaGlnAspLeuAlaGlnSerLeuAsp 61  
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QY	82	LysGlyLysLisAspIleAsp-----SerAspSerIleGlyLysThrPheAlaGly 98	QY	418	LeuGluLthrArgProSerSerArgArgLeuIleProMetProProAlaAspPheGly 437
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QY	99	LeuAspProAlaGlyAlaIleArgLysLisAspSerAlaArgAlaValGlyLysLysPro 118	QY	438	GlnThrValAlaAsnAsnProLysIleGluGluGluSerIleLeuLysGluThrLeuGly 457
Db	2302	CTAGACCCGGAGGGAGATACTACAGAGCTGGACGACGGG-----MAATCCC 2252	Db	1363	-----AACGCCAGAACATTCAGTTCACAACTAACAGAAACGAGGSCATTATG 1316
QY	139	ProValValThrAspValSerAlaProLeuAspGlyLysGluIleAspSerLeuIlePhe 158	QY	457	stryLeuValHisSerLysMetArgAsnProValPheGlnLeuThrProAlaSerSerPh 477
Db	2191	CGGGGACGTAATGCTACGAGCTACCGCTGGATGGGGGGACCTGGCCTACTAGTGATG 2132	Db	1315	CCTG-----AGGGTCAATCCCGTGTGAAATGACAT-GCGACGCTTA 1272
QY	159	SerPheProMetPheArgThrAlaIleValAlaAsnValAlaIleAsnValGluAsnLysGluMet 178	QY	477	egiyAlaValSerPheAsnAsnProGlyTyroGluArgThrArgAsp---LeuProAsp 496
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QY	179	SerLeuAspValValAsn---AspLeu-----IleGluIlePheAsnAsnLeu 193	QY	509	-----ThrAlaValAlaHis-PheArgSerLeuSerHisSerCysSerIleValThr 525
Db	2074	--GTCGAAGGAGACGAAACGCCATCTGGATGGTTCGGAAGGATGG---AACACAGG 2021	Db	1169	GTCGATGCCGEGPATGTCATCACGCTACCCACTGCAAGGCTGTCGACCGCTTCG 1110
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QY	214	TyrThrValArgIleArgValAlaAsnProThr-----TyrAspValProAspPro 230	QY	545	AHISALGlyLeuLeuLysAsnGluGluIleLeuCysLeuAlaAspAspLeuAlaThr 565
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QY	231	ThrGlu---GlyLeuValArgThrValSerAspTyArgLeuThrIleLysAlaIleThr 249	QY	565	gleuthrGlyValTyroAlaThrAspAsnIleAlaAlaValSerAlaPheAla 585
Db	1921	ACTCAACTGGGGTATCAGGGTACTCTGAGACTTACCGCTGACATCGAGCCGTCACA 1862	Db	1010	GCACCCATTCGCATACCGCAAGCATACACCGATTCGGCTCTTGGGCTCTATCCGGATGGTGC 951
QY	250	CysGluAlaAsnMetProThrIleValAspGlyGlyIlePheThrIleGlyGlyIleValAla 269	QY	585	asnAsnMetLeuSerSerValLeuIlysserGluAlaIleAsnThrProheGlyInPheAl 585
Db	1861	GGTACTCTCAAGCACCCACTCTCGIGAATCAGGGAGTGGCGTATCGCCGATTCGTC--- 1805	Db	950	CAAGACCTAGCCGAGATACCCVGC-----TATGGCATCA 914
QY	270	LeuThrProSerLeuProGlnTyAspValserGluAlaIleTyAlaIleIle 289	QY	605	yGluThrAlaValGlyAlaIleGlnSerGlyLeuAlaLysLeuProGlyIleLeuMetSe 625
Db	1804	--CAACCGGAGAAAGAACACACGAGAACCCGACATAGTACCGGGGACCCAA 1748	Db	913	-----GCACGGGAGTGGCGATGCGGTGAGGACTCATAGAGGACGCCGAGAG 861
QY	290	Thr-----PheAlaArgProSerSerAlaAlaAlaIleAlaIleAlaPhe 302	QY	625	rvalProGlyLysIleAlaAlaArgValArgAlaArgArgAlaArgArg----- 641
Db	1747	ACGGGGCGAACCTTACAGCTCGGGGGTCAGGCCGCAACTACATGAGATGAGC--- 1691	Db	860	TGTGCGCTGAAATTCACCTCGGAGAGGCCAACGAGAGGCCGAGCTGTGCGGAAT 801
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AE005131					
LOCUS	AE005131				
DEFINITION	Halobacterium sp. NRC-1 section 11659 bp DNA linear BCT 12-FEB-2001				
ACCESSION	AE005131 AE00437				
VERSION	AE005131.1 GI:10581942				
KEYWORDS	Halobacterium sp. NRC-1.				
SOURCE	Halobacterium sp. NRC-1.				
ORGANISM	Halobacteriaceae; Halobacterium.				
REFERENCE	1 (bases 1 to 1659)				
AUTHORS	Ng, W. V., Kennedy, S. P., Mahairas, G. G., Berquist, B., Pan, M., Shukla, H. D., Lasky, S. R., Baliga, N., Thorsson, V., Sbrooma, J., Swartzell, S., Weir, D., Hall, J., Dahl, T. A., Welti, R., Goode, Y. A., Leithauser, B., Kellie, K., Cruz, R., Danson, M. J., Hough, D. W., Maddocks, D. G., Jablonski, P. E., Krebs, M. P., Angevine, C. M., Dale, H.,				

Isenbarger, T.A., Peck, R.F., Pohlschrod, M., Spudich, J.L., Jung, K.-H., Alam, M., Freitas, M., Hou, S., Daniels, C.J., Dennis, P.P., Omer, A.D., Ebbhardt, H., Lowe, T.M., Liang, P., Riley, M., Hood, L. and DasSarma, S. Genome sequence of Halobacterium species NRC-1. *Proc. Natl. Acad. Sci. U.S.A.* 97 (22), 12176-12181 (2000)

**JOURNAL** **TITLE** **PUBLISHER** **REFERENCE** **AUTHORS** **PROC.** **NATL. ACADEM. SCI. U.S.A.** 97 (22), 12176-12181 (2000)

**FEATURES** **SOURCE** **TITLE** **JOURNAL** **PUBLISHED** **2** (bases 1 to 11659) **NG, W.V., Kennedy, S.P., Mahairas, G.G., Berquist, B., Pan, M., Shukla, H.D., Lasky, S.R., Baliga, N., Thorsson, V., Sbrocina, J., Swartzell, S., Weir, D., Hall, J., Dahl, T.A., Welti, R., Goo, Y.A., Leithauser, B., Kehler, K., Cruz, R., Danson, M.J., Hough, D.W., Maddocks, D.G., Jablonski, P.E., Krebs, M.P., Angevine, C.M., Dale, H., Isenbarger, T.A., Peck, R.F., Pohlschrod, M., Spudich, J.L., Jung, K.-H., Alam, M., Freitas, T., Hou, S., Daniels, C.J., Dennis, P.P., Omer, A.D., Ebbhardt, H., Lowe, T.M., Liang, P., Riley, M., Hood, L. and DasSarma, S. Direct Submission**

Submitted (14-JUL-2000) Institute for Systems Biology, 4225 Roosevelt Way NE, Seattle, WA 98105, USA

**FEATURES** **SOURCE** **1** (bases 1 to 11659) **/organism="Halobacterium sp. NRC-1"** **/strain="NRC-1"** **/db\_xref="taxon:64091"** **gene** **157..1074** **/gene="Yfec"** **/note="Yfec"** **/codon\_start=1** **/transl\_table=11** **/product="6-phosphoglucanate dehydrogenase"** **/protein\_id="ANG20506.1"** **/db\_xref="GI:10581943"** **/translation="MELGVGLGRMGRTIVDRCDAQHGVAFIDATAREDAADAGATPADDLALAKELGAERKTRWLMVPGDPVDADELAQPHSDDDVVVGNSHEDSTRRAEBHDFAVTLDCGTGGPAGELFSLMLGGPWWAYDLPVPAVATGGDGRMGPGAGCHYKRMHVEALMOTYGGELLHGRYDLEAVARTWINGVAVRNLLELCSEAREECSDDLGIVDHRAGGSIGTWTQVQALEQEVPVPLVQALSERFSGSASTGGDTGRFARRLNLRLRGFGHRREVAFNGDDA" complement(1071..1652)**

**gene** **VNG2554H** **/gene="VNG2554H"** **/note="hypothetical protein"** **/codon\_start=1** **/transl\_table=11** **/product="Yfec"** **/note="hypothetical protein"** **/db\_xref="GI:10581944"** **/translation="MDVAVLLEPFGEDELDAIGPMVFRPAELGGDLDVSMRMLVDEGVTAKHGLIVAPDQVPLFGVPLDVLVPGGGWTTDRPQWSEVERETPLPRLDTTHGGTAGDLALHVERECCSAGLAQAEQVATEIESTY" complement(1746..2324)**

**gene** **VNG2555C** **/db\_xref="GI:10581945"** **/translation="MVTGTYVTLGIGVTLFVWVHLAKGSSKPPAEDIAQDVLLEHRASVTPEDPERNSIGGGGAGAVAGGAELSELERGEEDDDGFEDDAIADDVEYEIEYKEGETELVANSISLDLGVDESDLPLPACQQCQCVSCSGRVADGEDAAEYIRHSNNESLGDAELEBEGGMCTCAHTSFSIETDEP" complement(2413..2485)**

**gene** **VNG2556H** **/note="hypothetical protein"** **/db\_xref="GI:10581946"** **/translation="MVTDQGLLAVGGVNLAVMTLHSQPIITAAADQSGGLGVLIWAVLWLGFLGLAVGTYWADGAVCPILATGTLGACIWLNGITAPPSESTLSVBAWPFLVLWVVGIAEQUITGHAVDSNRSSQE" complement(3099..4019)**

**gene** **VNG2556H** **/note="hypothetical protein"** **/db\_xref="GI:10581947"** **/translation="MVTQPANDANGCTPDRGLSGCTDLYVRYPGGDPVIGESVTVPVGDVVALIGNGSGESTLNLANKHSRPAQGFTVLDGHITDELGSKELARRGLLSQGOKQWIMWAMALQDPTVLLDEPTEFLDHQHQLVMDLQALRHDH"WWVHLIDINQARIAHDVIALKGDTIHKRGPAQDVVKETLRTVFDITATVSTISHGMQVWPIEALHDEDGIDHEHAPGSRPTEFADSGCTPPAE" complement(4023..5102)**

**gene** **VNG2560G** **/note="YfmD2"** **/db\_xref="GI:1051948"** **/translation="MVTQPEWLSACQWTRATLGLGOLPMILRWSQWVNRWPLRPTVGLVAGLAWSGWHVTPDEPEWLSACQWTRATLGLGOLPMILRWSQWVNRWPLRPTVGLVAGLAWSGAIFQVTRNELASVYIWSVAGMVLILTLEFSQVPMQPLAIGLAVIILVATWNGTNPVRLVLAGVWVTSVRSVQRLAFFDNLG3VMSAQTWLGSLLQDWAQVIALPFTVLSLAFLAFTWNEVDLILBETASLGMVPEVKRFGVAAIAIUSTAAITVAGLIGVGGYFLTLMRTRVNLGLI" complement(5109..6263)**

**gene** **VNG2562H** **/note="YfmD2"** **/db\_xref="GI:1051949"** **/translation="MARRQIQLAGGASLJAASLAGCTTQSPTDGGSTQTQDAGDSVTVVEPNPPTIFESVPEYTAIPSVWMMGMAQIOPRATASGRAPHKFKYDLPDVFRKATIEQIADSRSQYGRNFYADCDVHLDPRMLFYANWMDDAIESSGAPMGSSTRFASSAVGDGPFDLYAEFKASSFETFORRAREAWOSKADIMTSGLPPEESDRPITVAIWRGRWPDGQFRIAPLDDQDNQNTLYRLGMDQAFAGAVPDRGIGYERLDDPDYGAVGCLTSOPHAEFDUTWEPFEEANPQGQOLTAENGIVNURTSQOFMGPTDIFSTEAQAKMYPDQFPGSWGSPTEIPASERLFDRQVRVDAINGVGL" complement(6353..7216)**

**gene** **VNG2563H** **/note="hypothetical protein"** **/db\_xref="GI:10581949"** **/translation="MARRQIQLAGGASLJAASLAGCTTQSPTDGGSTQTQDAGDSVTVVEPNPPTIFESVPEYTAIPSVWMMGMAQIOPRATASGRAPHKFKYDLPDVFRKATIEQIADSRSQYGRNFYADCDVHLDPRMLFYANWMDDAIESSGAPMGSSTRFASSAVGDGPFDLYAEFKASSFETFORRAREAWOSKADIMTSGLPPEESDRPITVAIWRGRWPDGQFRIAPLDDQDNQNTLYRLGMDQAFAGAVPDRGIGYERLDDPDYGAVGCLTSOPHAEFDUTWEPFEEANPQGQOLTAENGIVNURTSQOFMGPTDIFSTEAQAKMYPDQFPGSWGSPTEIPASERLFDRQVRVDAINGVGL" complement(6353..7216)**

**gene** **VNG2564H** **/note="hypothetical protein"**



QY	368	rAlaGlyAlaPheThrVal---ThrPheArgGlnValAlaValAlaPheGluValValValThrAs	387
Db	1482	GTGGGGCGACACCGTGAGGCGCTGGCGCCGCGCTCGCG	1515
QY	387	nasnProAlaGlyGlyGlySerAlaProThrPheThrValArgValProProSerAsnI	407
Db	1516	-AGCCCTGCTGGCGACAGCGCTGGCATCGACAGCTCGAGGTCCGCCAGCTCGC	1574
QY	407	aTyThrThrAsnThrValPheArgAsnThrLeuLeu-----GlutThrAs	421
Db	1575	G-----GCCGTGGCGAACCTCTACGGCCGATGGCGTCAGTCGTCGA	1622
QY	421	gProSerSerArgArg-LeuGluLeuProMetProProAlaAspPheGlyGlnThrValA	441
Db	1623		1666
QY	441	laasnAsnProLySleGluGlnSerLeuLeuLysGluThrLeuGlyCysTyrLeuValH	461
Db	1667	--CCACACCTCTCAA-----	1678
QY	461	lSerLysMetArgAsnProValPheGlnLeuThrProAlaSerSerPheGlyAlaValA	481
Db	1678	-----	1678
QY	481	erPheAsnAsnProGlyTygGluArgThrArgAspLeuProAspTygThrGlyLeargA	501
Db	1679	:     -----AATTCGCCCGGA-----	1691
QY	501	spSerPheAspGlnAsnMetSerThrAlaValAlaHisPheArgSerLeuSerHisSerC	521
Db	1692	AAACGTTGGTGCAGCAATCACAACTACTGTGTTAACTCTGCTTCATACCGCTAACGCTAGTT	1751
QY	521	ySsErLeValThrLysThrTygGlnGlyTriPheGlyValThrAsnValAsnThrProP	541
Db	1752	ACACACTGGTGTACCGCTGGCTGG-----GGTGAACATGTTGTCGTCGCTC-----	1804
QY	541	heGlyGlnPheAlaHisAlaLysGlyLeuLeuLys-----AsnGluLysIleucySleu	558
Db	1805	-----GCATCTCGCGAGGGCTCATCAAGGCCGCCGGGAGGACATC-----	1847
QY	559	AlaAspAspPheAlaThrArgLeuThrGlyValTyrProAlaThrAsp-AsnPhe-----	576
Db	1848	GCACAGGAGCTCCCTCGAACACCGTGCGTCACAGTGCCGGAGACGGACTTCCCTGAGCCG	1907
QY	577	-----AlaAlaAlaValSerAlaPheAlaAlaAlaAsnMe	587
Db	1908	TACAAACCGCTCCATGGGGCGGGGGGGCGCGCGCTGCGCTGGCGGCCGAGTCG	1967
QY	587	tLeuSerSerValLeuLysSerGluAlaThrSerSerSerIleLeuLysSerValGlyGluH	607
Db	1968	GAACTCGAGAACGCGCGAGGAGGAAGACGAGGCTCTGATCCGGACCGATGCCGAGAC	2027
QY	607	ralavalGlyAlaLysGlyLeuAlaLysLeuProGlyLeuLeuMetSerValPr	627
Db	2028	GAAGTCGAGTACTACGAGATCAGTCAGTCAGCAGCAAGG-----	2061
QY	627	oGlyLysIleAlaLalaArgValAlaGlyArgGalaArgGalaAlaArgAla	647
Db	2062	-----AAGGCGAGACCATCGAGGTCGCGAGCAAGGAGAGCATC	2099
QY	647	n 647	:
Db	2100	C 2100	:

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